AMENDMENTS TO THE CLAIMS

Please enter the following amendments:

1. **(Withdrawn)** A method of constructing an apparatus for identifying a pathogenic agent in a sample, comprising

providing a set of host cells and contacting the cells with the pathogenic agent or any sample containing pathogenic agent,

employing a microarray having a plurality of probes to measure a plurality of biological responses of the host cells,

applying the measured plural biological responses to train a machine learning system to recognize a pathogenic agent, and

detecting and identifying a pathogenic agent in a sample, by exposing host cells to said sample, using a microarray to measure plural biological responses provoked in host cells, and employing the trained machine learning system to identify the pathogenic agent.

2. **(Withdrawn)** A method according to claim 1, further comprising

employing the set of host cells and a plurality of microarrays to increase a plurality of biological responses available to the identification process, and

applying machine learning to said plural biological responses to identify a pathogenic signature.

3. **(Withdrawn)** A method according to claim 2, further comprising

providing a plurality of sets of host cells,

contacting said host cells with a sample containing pathogenic agents to provoke and measure a plurality of biological responses,

training a recognizer to detect one or more of said pathogenic signatures in a biological response provoked in a host cell, and

applying machine learning to said plural respective biological responses to identify at least one pathogenic signature.

4. **(Withdrawn)** A method according to claim 1, further comprising

wherein the pathogenic agent to be identified is contained within an environmental sample that contains other substances and/or pathogenic agents.

5. **(Withdrawn)** A method according to claim 1, further comprising

employing substantially all of the measured biological response data during the identification method to widen the scope of information employed during pathogen detection.

6-9. **(Cancelled)**

10. **(Withdrawn)** A method according to claim 1, further comprising

employing the similarity of the host cell response to pathogenic agents that represent different strains of the same pathogen, altered pathogens, genetically engineered pathogens, and/or mutated pathogens,

wherein the host cells act as a natural filtering mechanism allowing identification of the pathogenic agents that differ from the agents used for training

11. **(Withdrawn)** A method according to claim 1, wherein

employing a microarray includes employing a microarray having a uniform set of probes.

12-13. **(Cancelled)**

14. **(Withdrawn)** A method according to claim 1, wherein the host cells include cultured host cells and/or host cells grown from cell lines.

15. **(Withdrawn)** A method according to claim 1, wherein the host cells include host cells of different types

16. **(Withdrawn)** A method according to claim 1, wherein host cells include cells selected from different organisms or species.

17-18. **(Cancelled)**

19. **(Withdrawn)** The method according to claim 1, wherein the pathogenic agent includes substances and/or stimuli capable of eliciting a response in the host cell.

20. **(Withdrawn)** The method of claim 1, wherein the sample is derived from a human or animal, and wherein the sample is selected from the group consisting of blood, urine, feces, sputum, saliva, semen, vaginal fluid, cerebrospinal fluid, skin cells, hair follicles, bone fragments, bone marrow, brain matter, and amniotic fluid.

21. **(Withdrawn)** The method of claim 1, wherein the sample is derived from an environmental or industrial matter.

22. **(Withdrawn)** The method of claim 1, wherein the sample consists of gas, liquid, or solid, or combinations of these states.

23. **(Withdrawn)** The method of claim 1, wherein the sample is selected from the group of air, water, and soil.

24. **(Withdrawn)** The method of claim 1, wherein the host cells comprise a cell selected from the group of lung, skin, nerve, and immune system.

25. **(Withdrawn)** The method of claim 1, wherein the one or more biological responses of the host cells comprise genomic microarray data of the host cell response.

26. **(Withdrawn)** The method of claim 1, wherein the one or more biological responses of the host cells comprise proteomic microarray data of the host cell response.

27. **(Withdrawn)** The method of claim 1, wherein the one or more biological responses of the host cells comprise both genomic microarray data and proteomic microarray data.

28. **(Withdrawn)** The method of claim 1, wherein the one or biological responses of the host cells comprise genomic, proteomic, metabolomic and fusion thereof.

29. **(Withdrawn)** The method of claim 1, wherein the microarrays include microarrays having non-uniform probe sets, or multiple microarrays having different sets of probes.

30-34. **(Cancelled)**

35. **(Withdrawn)** The method of claim 7,

wherein fusing includes weighting candidate identification responses.

36. **(Currently amended)** A method for identifying ~~the presence of~~ a pathogenic agent, comprising

collecting ~~disparate types of~~ biological data representative of a biological response to the ~~same~~ pathogenic agent, and

employing information fusion to process the biological response [[.]] ,

to identify a pathogenic agent.

37. **(Currently amended)** The method of claim 36, including the further step of

collecting multiple modalities of biological data representative of a biological response to the ~~same~~ pathogenic agent.

38. **(Currently amended)** The method of claim 36, wherein collecting data includes employing at least one microarray[[s]] each having [[a]] at least one set of probes.

39. **(Currently amended)** The method of claim 36, further comprising

applying machine learning to process the biological data and to develop a signature for the

~~pathogen~~ pathogenic agent that includes substantially all of the data collected by common probes among the microarrays.

40. **(Original)** The method of claim 36, wherein

the biological response include the biological response of a host cell.

41-46. **(Cancelled)**

47. **(Currently amended)** ~~The~~ A method for identifying a pathogenic agent according to ~~of~~ claim 36, wherein the step comprising collecting ~~disparate types of~~ biological data representative of a biological response comprises

providing a set of host cells and contacting the cells with the pathogenic agent or any sample containing pathogenic agent and

employing a microarray having a plurality of probes to measure and collect a plurality of biological responses of the host cells,

and wherein the method for identifying a pathogenic agent further includes

applying the ~~measured plural~~ plurality of biological responses of the host cells to train a machine learning system to recognize the pathogenic agent and

detecting and identifying the pathogenic agent in a sample, by exposing host cells to said sample, using a microarray to measure plural biological responses provoked in host cells, and employing the trained machine learning system to identify the pathogenic agent.

48. **(Currently amended)** The method of claim 47, further comprising

employing the set of host cells and a plurality of microarrays to increase a plurality of biological responses ~~available to the identification process~~, and

applying machine learning to said ~~plural~~ plurality of biological responses to identify a pathogenic signature.

49. **(Currently amended)** The method of claim 48, further comprising

providing a plurality of sets of host cells,

contacting said host cells with a sample containing pathogenic agents to provoke and measure a plurality of biological responses,

training a recognizer to detect one or more of said pathogenic signatures in a biological response provoked in a host cell, and

applying machine learning to said ~~plural respective~~ plurality of biological responses to identify at least one pathogenic signature.

50. **(Previously presented)** The method of claim 47, further comprising

employing substantially all of the measured biological response data during the identification method to widen the scope of information employed during pathogen detection.

51. **(Currently amended)** The method of claim 50 ~~47~~, wherein

employing substantially all of the measured biological response data includes identifying a pathogen signature having substantially all of the measured biological data.

52. **(Previously presented)** The method of claim 49, further comprising

allowing the recognizer to generate plural decision results, and

fusing said plural decision results to generate a determination of the identity of a pathogen in a test sample.

53. **(Currently amended)** The method of claim 47, further comprising

using the host cells as a natural amplification mechanism, ~~wherein the host cell response to an agent of high virulence is vigorous,~~ thereby allowing improved detection and identification of pathogenic agents.

54. **(Previously presented)** The method of claim 47, wherein

employing a microarray includes employing microarrays of different modalities.

55. (**Previously presented**) The method of claim 54, wherein the different modalities include modalities selected from the group consisting of genomic, proteomic, and metabolomic.

56. (**Previously presented**) The method of claim 47, wherein the pathogenic agent is a non-nucleic-acid-containing pathogenic agent.

57. (**Previously presented**) The method of claim 56, wherein the non-nucleic-acid-containing pathogenic agent is a toxin.

58. (**Currently amended**) The method of claim 47, further comprising

fusing information from at least one of: multiple types ~~and/or species~~ of host cells, multiple species of host cells, multiple microarray types, multiple ~~and/or disparate~~ sets of probes, ~~and/~~or multiple modalities.

59. (**Previously presented**) The method of claim 47, further comprising

fusing multiple candidate identification responses generated by multiple classifiers.

60. (**Previously presented**) The method of claim 47, further comprising

partitioning an input space of microarray probes into one or more computational subspaces and generating measures of fitness for said subspaces.

61. (**Previously presented**) The method of claim 47, further comprising

generating multiple measures of fitness within a subspace wherein intra-subspace measures of fitness are dynamic having a value depending on the region within the subspace and position within the subspace of a point representing the test sample

62. (**Previously presented**) The method of claim 60, further comprising determining for a subspace a fitness measure representative of an effectiveness of a classifier operating in the respective subspace.

63. **(Previously presented)** The method of claim 47, wherein analyzing a data set includes partitioning an input space into plurality of subspaces.

64. **(Previously presented)** The method of claim 63, further comprising fusing measures of recognition generated from respective areas of said subspaces.

65. **(Previously presented)** The method of claim 64, further comprising using subspace measures of fitness and fusing multiple classifiers.

66. **(Previously presented)** The method of claim 65, further comprising applying Dempster-Shafer theory of evidence for fusing multiple classifiers.

67. **(New)** The method of claim 36, wherein the pathogenic agent is uncataloged.

68. **(New)** A method for identifying a pathogenic agent, comprising

collecting biological data representative of a biological response of host cells to the pathogenic agent,

applying the biological data to train a machine learning system to recognize the pathogenic agent, and

employing the trained machine learning system to identify the pathogenic agent.